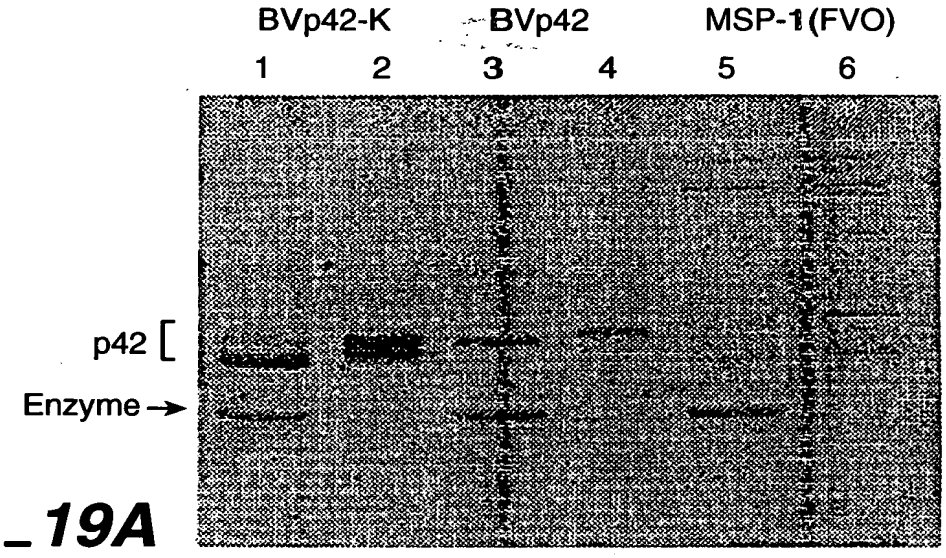


FIG._19A

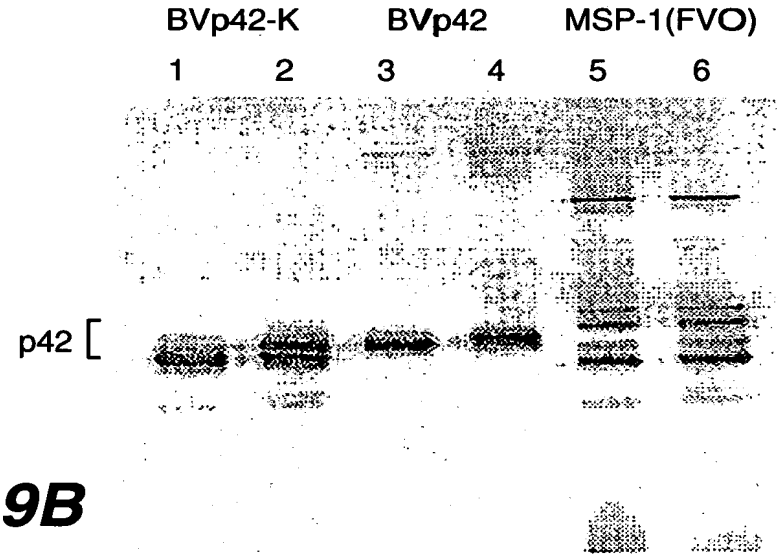


FIG._19B

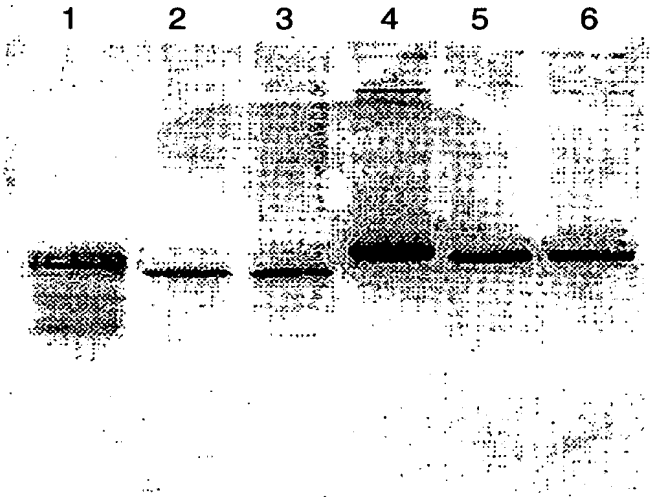


FIG._20

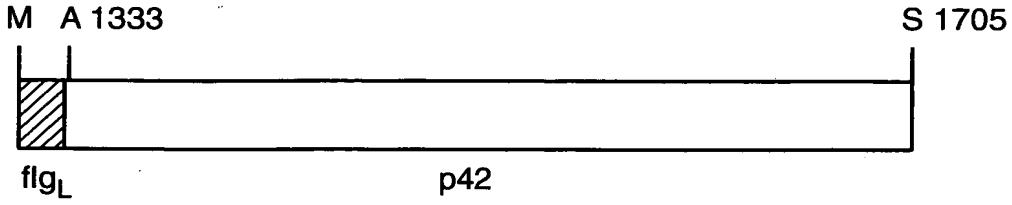


FIG._1A

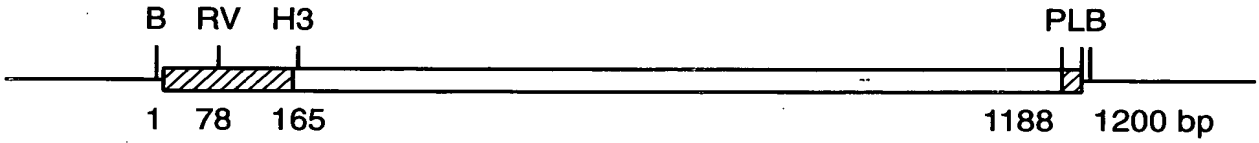


FIG._1B

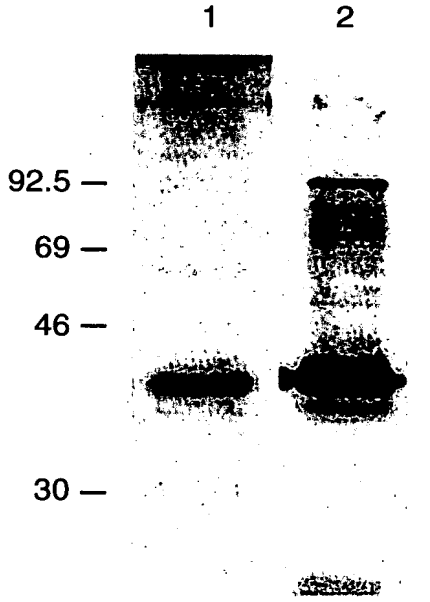


FIG._2A

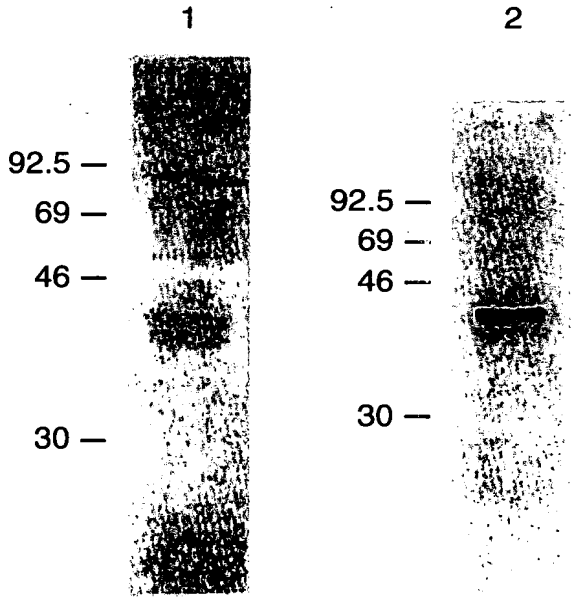


FIG._2B

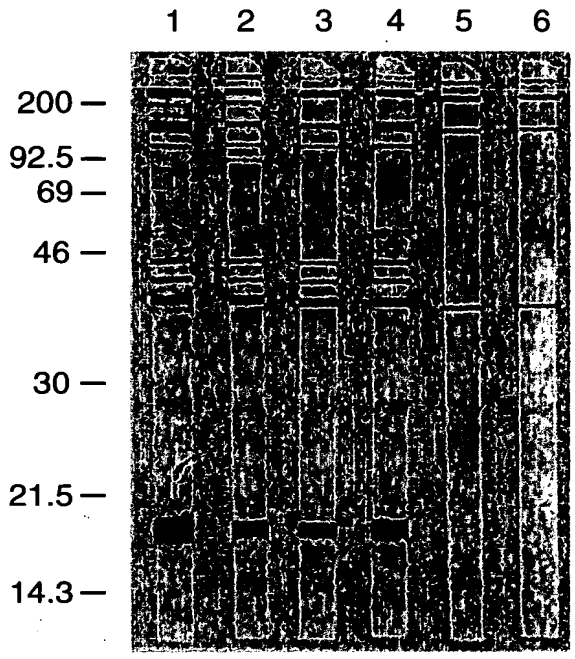


FIG._3A

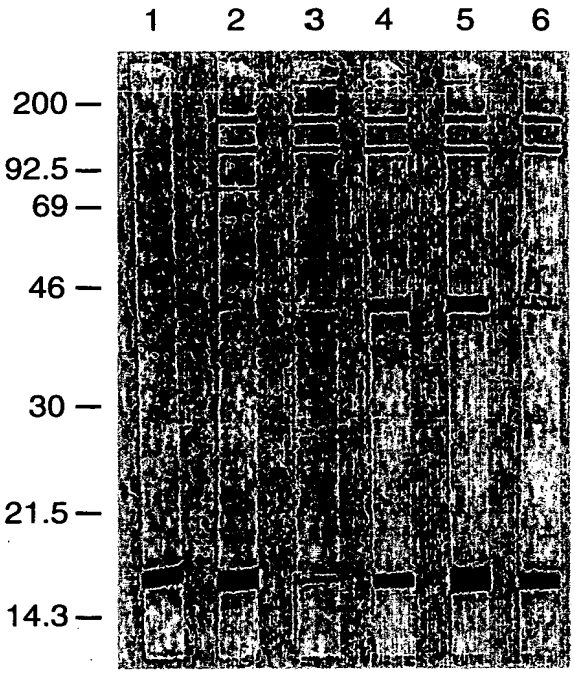


FIG._3B

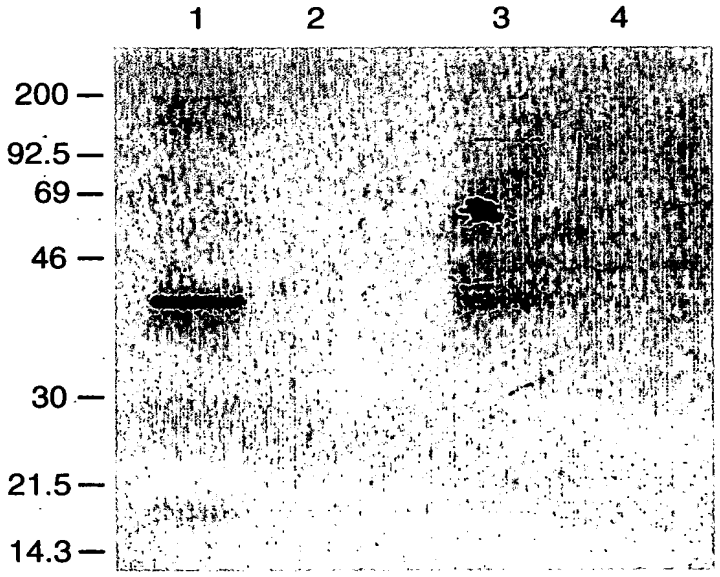


FIG._3C

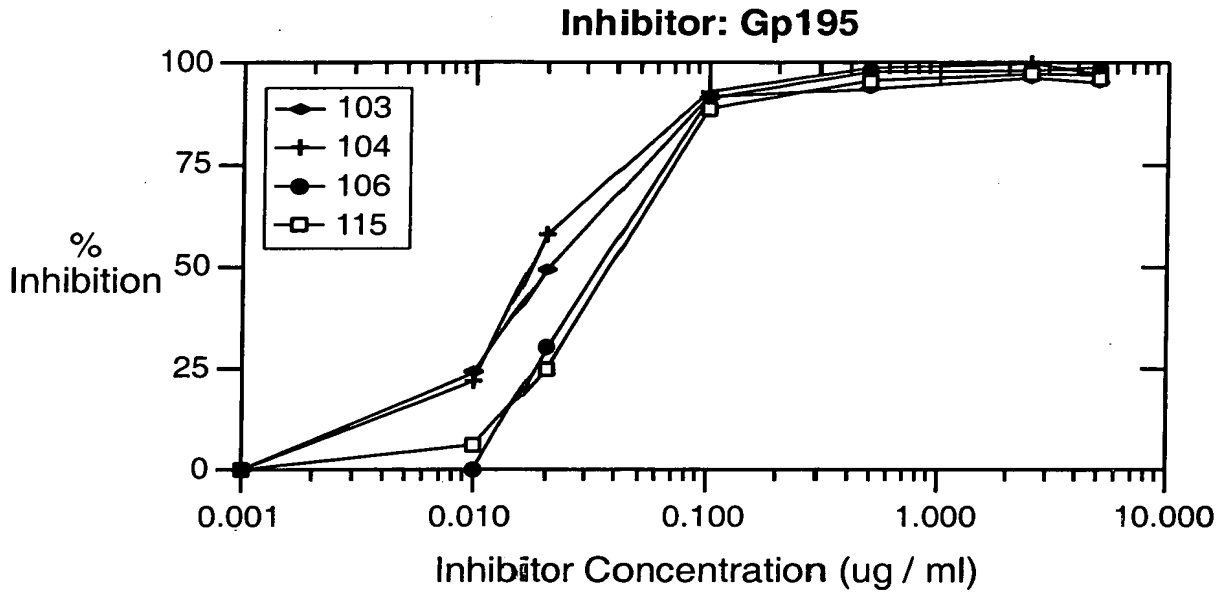


FIG._4A

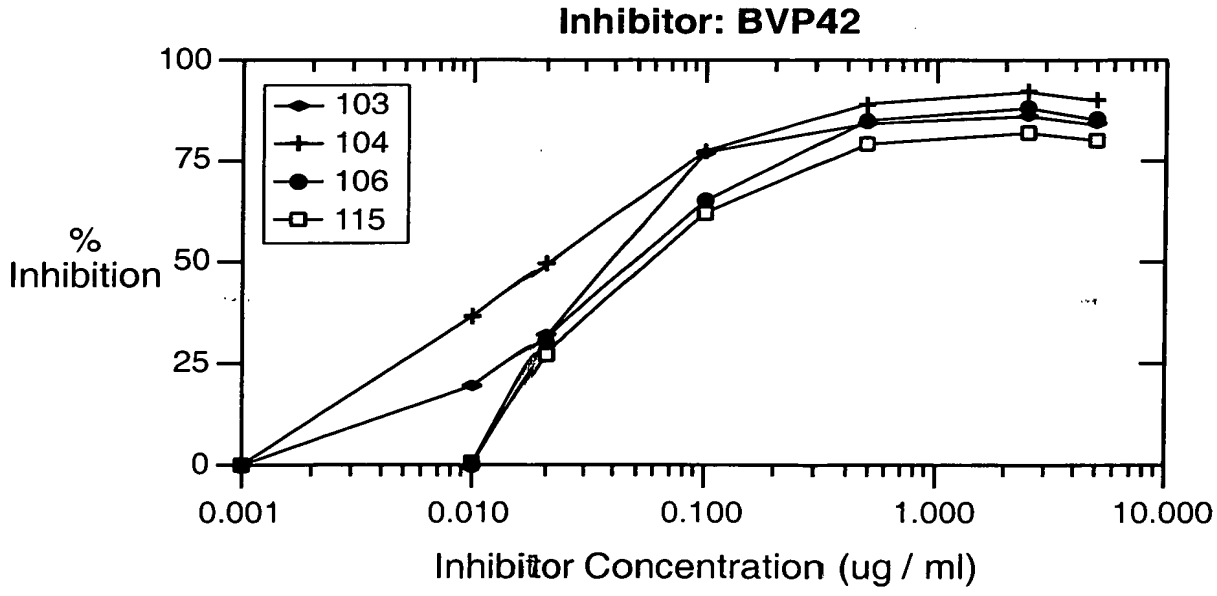


FIG._4B

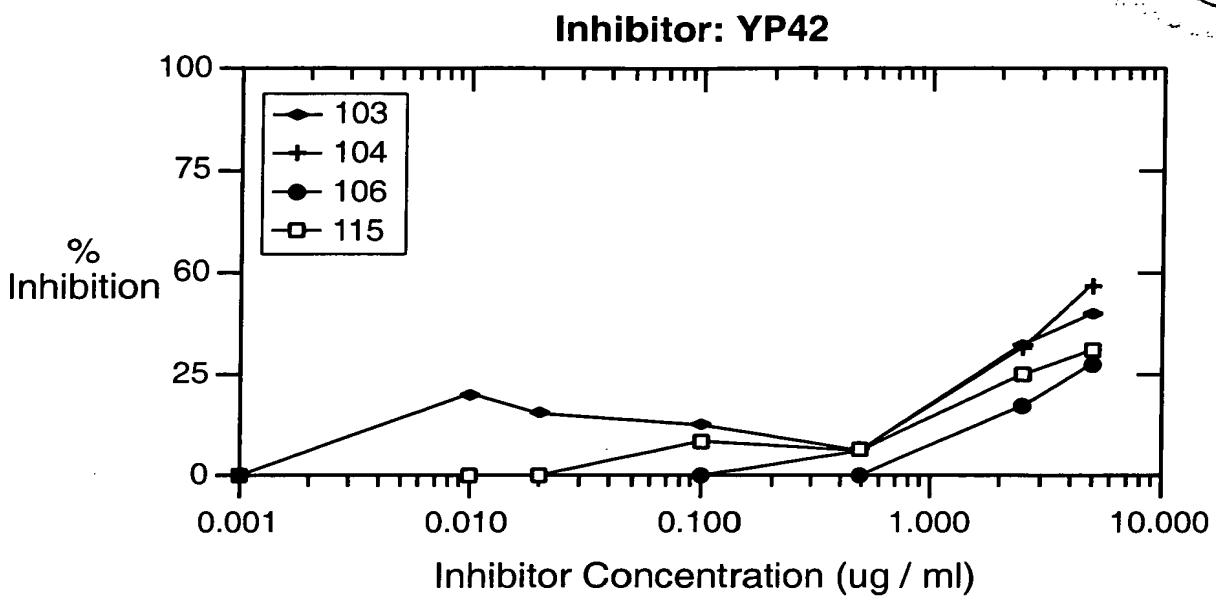


FIG._4C

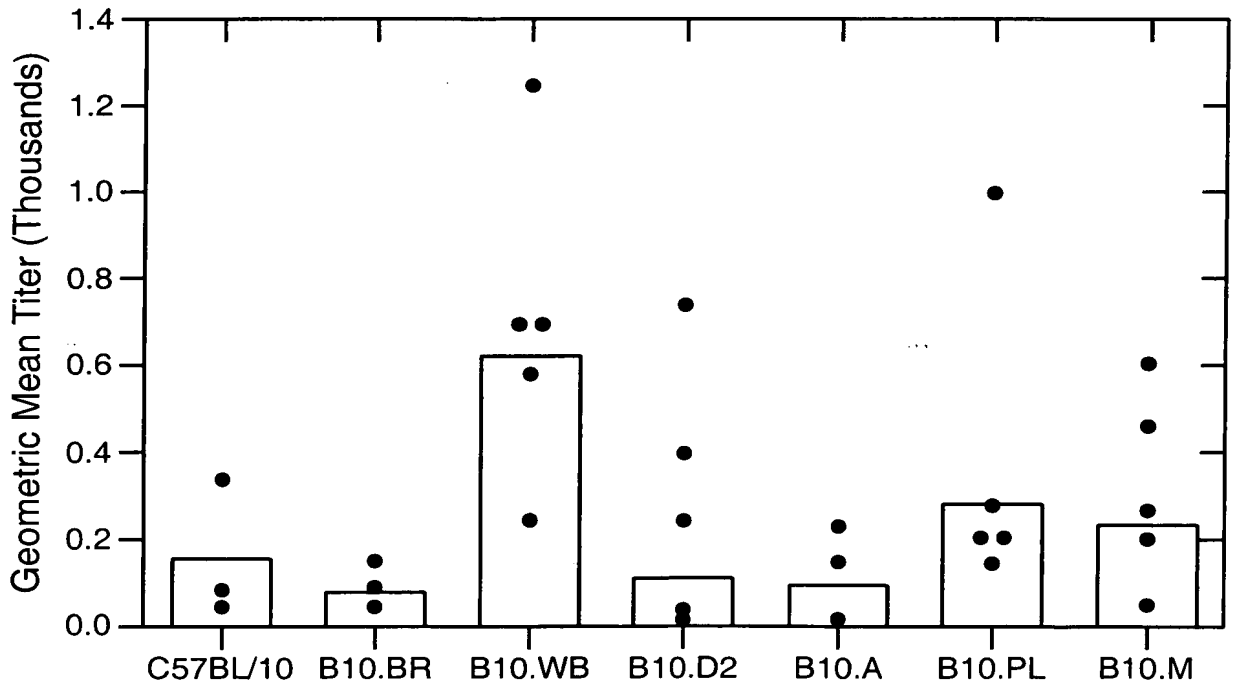
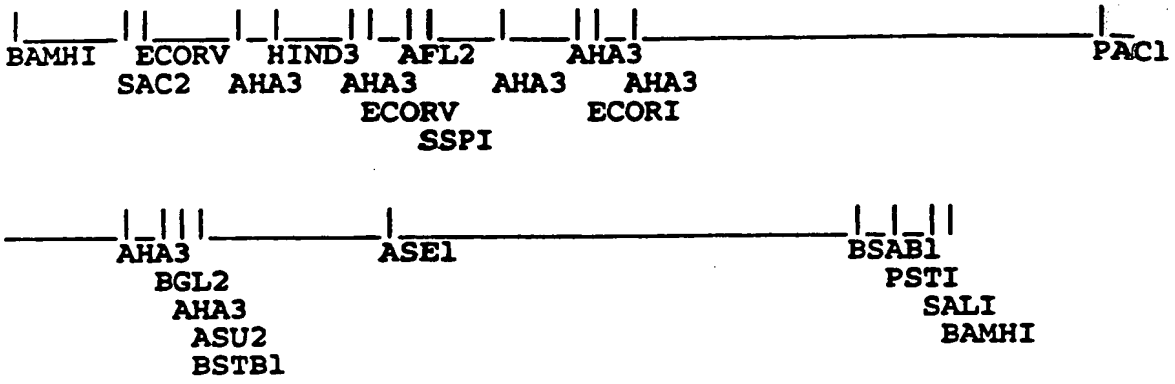


FIG._5

```
FUP  AISVT.MDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKYFLDVLESDLM  1402
MAD                                          I                                 1377
WEL   VTTSVI     KI    E L               L N VM   V VK      FN  EN KN      I  1384
 K1   VTPSVIH    KI    E L               L N VM   V VK     PFN  EN KN      I  1325

FUP  QFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGISYYEKVLAKYKDDLESIKKVIK  1473
MAD                          I                                                 1448
WEL  PY DLT SN VVK PY F  K KRDKF S  N   D IDT  N  NDVLG  KILSE   S  D    Y N  1405
 K1  PY DLT SN VVK PY F  K KRDKF S  N   D IDT  N  NDVLG  KILSE   S  D    Y N  1396

                                                                  ◇∞
FUP  EEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETLYNNLVNKIDDYLINLKAKINDCNVEKDEAHVK  1544
MAD                                                                            1519
WEL  ..................... K GENE Y    N      KTVND   LFV H E  VLNYTY  SNVE   1456
 K1  ..................... K GENE Y    N      KTVND   LFV H E  VLNYTY  SNVE   1447

                                                                        ◇
FUP  ITKLSDLKAIDDKIDLFKNHNDFEAIKKLINDDTKKDMLGKLLSTGLV.QNFPNTIISKLIEGKFQDML.N  1613
MAD                        T                              I                    1588
WEL   KE NY  T Q  LAD  KN N VG AD ST YNHNNL T F    M FE LLKSVL N LDW LARYVKH  1527
 K1   KE IY  T Q  LAD  KN N VG AD ST YNHNNL T F    M FE LLKS L N LDW LARYVKH  1518

       o   o     •         • •          •    ♦  •      •     •
FUP  ISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGK  1684
MAD                                          E                 T        SR   1659
WEL  FTTPMRK TMIQQS                                                          1598
 K1  FTTPMRK TMIQQ                        S                                  1589

      • •   o        •   →
FUP  KITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI                               1726
MAD                                                                           1701
WEL           C                                                               1640
 K1     Q         SMV                                                         1631
```

FIG._6




```
                  MetTrpSerTrpLysCysLeuLeuPheTrpAlaValLeuValThrAla
  1 GGATCCACTGGGATGTGGAGCTGGAAGTGCCTCCTCTTCTGGGCTGTCCTGGTCACAGCC
    CCTAGGTGACCCTACACCTCGACCTTCACGGAGGAGAAGACCCGACAGGACCAGTGTCGG

    1 BAMHI,

                  V
    ThrLeuCysThrAlaAlaIleSerValThrMetAspAsnIleLeuSerGlyPheGluAsn
 61 ACACTCTGCACCGCGGCGATATCTGTCACAATGGATAATATCCTCTCAGGATTTGAAAAT
    TGTGAGACGTGGCGCCGCTATAGACAGTGTTACCTATTATAGGAGAGTCCTAAACTTTTA

    71 SAC2, 78 ECORV,

    GluTyrAspValIleTyrLeuLysProLeuAlaGlyValTyrArgSerLeuLysLysGln
121 GAATATGATGTTATATATTTAAAACCTTTAGCTGGAGTATATAGAAGCTTAAAAAAACAA
    CTTATACTACAATATATAAATTTTGGAAATCGACCTCATATATCTTCGAATTTTTTTGTT

    138 AHA3, 165 HIND3,

    IleGluLysAsnIlePheThrPheAsnLeuAsnLeuAsnAspIleLeuAsnSerArgLeu
181 ATTGAAAAAAACATTTTTACATTTAATTTAAATTTGAACGATATCTTAAATTCACGTCTT
    TAACTTTTTTTGTAAAAATGTAAATTAAATTTAAACTTGCTATAGAATTTAAGTGCAGAA

    207 AHA3, 220 ECORV, 238 AFL2,

    LysLysArgLysTyrPheLeuAspValLeuGluSerAspLeuMetGlnPheLysHisIle
241 AAGAAACGAAAATATTTCTTAGATGTATTAGAATCTGATTTAATGCAATTTAAACATATA
    TTCTTTGCTTTTATAAAGAATCTACATAATCTTAGACTAAATTACGTTAAATTTGTATAT

    251 SSPI, 289 AHA3,

    SerSerAsnGluTyrIleIleGluAspSerPheLysLeuLeuAsnSerGluGlnLysAsn
```

FIG._7A

```
301  TCCTCAAATGAATACATTATTGAAGATTCATTTAAATTATTGAATTCAGAACAAAAAAAC
     AGGAGTTTACTTATGTAATAACTTCTAAGTAAATTTAATAACTTAAGTCTTGTTTTTTTG

     331 AHA3, 342 ECORI,

     ThrLeuLeuLysSerTyrLysTyrIleLysGluSerValGluAsnAspIleLysPheAla
361  ACACTTTTAAAAAGTTACAAATATATAAAAGAATCAGTAGAAAATGATATTAAATTTGCA
     TGTGAAAATTTTTCAATGTTTATATATTTTCTTAGTCATCTTTTACTATAATTTAAACGT

     366 AHA3,

     GlnGluGlyIleSerTyrTyrGluLysValLeuAlaLysTyrLysAspAspLeuGluSer
421  CAGGAAGGTATAAGTTATTATGAAAAGGTTTTAGCGAAATATAAGGATGATTTAGAATCA
     GTCCTTCCATATTCAATAATACTTTTCCAAAATCGCTTTATATTCCTACTAAATCTTAGT

     IleLysLysValIleLysGluGluLysGluLysPheProSerSerProProThrThrPro
481  ATTAAAAAAGTTATCAAAGAAGAAAAGGAGAAGTTCCCATCATCACCACCAACAACACCT
     TAATTTTTTCAATAGTTTCTTCTTTTCCTCTTCAAGGGTAGTAGTGGTGGTTGTTGTGGA

     ProSerProAlaLysThrAspGluGlnLysLysGluSerLysPheLeuProPheLeuThr
541  CCGTCACCAGCAAAAACAGACGAACAAAAGAAGGAAAGTAAGTTCCTTCCATTTTTAACA
     GGCAGTGGTCGTTTTTGTCTGCTTGTTTTCTTCCTTTCATTCAAGGAAGGTAAAAATTGT

     AsnIleGluThrLeuTyrAsnAsnLeuValAsnLysIleAspAspTyrLeuIleAsnLeu
601  AACATTGAGACCTTATACAATAACTTAGTTAATAAAATTGACGATTACTTAATTAACTTA
     TTGTAACTCTGGAATATGTTATTGAATCAATTATTTTAACTGCTAATGAATTAATTGAAT

     649 PAC1,

     LysAlaLysIleAsnAspCysAsnValGluLysAspGluAlaHisValLysIleThrLys
661  AAGGCAAAGATTAACGATTGTAATGTTGAAAAAGATGAAGCACATGTTAAAATAACTAAA
     TTCCGTTTCTAATTGCTAACATTACAACTTTTTCTACTTCGTGTACAATTTTATTGATTT

     LeuSerAspLeuLysAlaIleAspAspLysIleAspLeuPheLysAsnHisAsnAspPhe
721  CTTAGTGATTTAAAAGCAATTGATGACAAAATAGATCTTTTTAAAAACCATAACGACTTC
     GAATCACTAAATTTTCGTTAACTACTGTTTTATCTAGAAAAATTTTTGGTATTGCTGAAG

     729 AHA3, 753 BGL2, 760 AHA3, 778 ASU2 BSTB1,

     GluAlaIleLysLysLeuIleAsnAspAspThrLysLysAspMetLeuGlyLysLeuLeu
781  GAAGCAATTAAAAAATTGATAAATGATGATACGAAAAAAGATATGCTTGGCAAATTACTT
     CTTCGTTAATTTTTTAACTATTTACTACTATGCTTTTTTCTATACGAACCGTTTAATGAA

     SerThrGlyLeuValGlnAsnPheProAsnThrIleIleSerLysLeuIleGluGlyLys
841  AGTACAGGATTAGTTCAAAATTTTCCTAATACAATAATATCAAAATTAATTGAAGGAAAA
     TCATGTCCTAATCAAGTTTTAAAAGGATTATGTTATTATAGTTTTAATTAACTTCCTTTT

     885 ASE1,

     PheGlnAspMetLeuAsnIleSerGlnHisGlnCysValLysLysGlnCysProGluAsn
901  TTCCAAGATATGTTAAACATTTCACAACACCAATGCGTAAAAAAACAATGTCCAGAAAAT
     AAGGTTCTATACAATTTGTAAAGTGTTGTGGTTACGCATTTTTTTGTTACAGGTCTTTTA

     SerGlyCysPheArgHisLeuAspGluArgGluGluCysLysCysLeuLeuAsnTyrLys
961  TCTGGATGTTTCAGACATTTAGATGAAAGAGAAGAATGTAAATGTTTATTAAATTACAAA
     AGACCTACAAAGTCTGTAAATCTACTTTCTCTTCTTACATTTACAAATAATTTAATGTTT
```

FIG._7B

```
      GlnGluGlyAspLysCysValGluAsnProAsnProThrCysAsnGluAsnAsnGlyGly
1021  CAAGAAGGTGATAAATGTGTTGAAAATCCAAATCCTACTTGTAACGAAAATAATGGTGGA
      GTTCTTCCACTATTTACACAACTTTTAGGTTTAGGATGAACATTGCTTTTATTACCACCT

      CysAspAlaAspAlaLysCysThrGluGluAspSerGlySerAsnGlyLysLysIleThr
1081  TGTGATGCAGATGCCAAATGTACCGAAGAAGATTCAGGTAGCAACGGAAAGAAAATCACA
      ACACTACGTCTACGGTTTACATGGCTTCTTCTAAGTCCATCGTTGCCTTTCTTTTAGTGT

      CysGluCysThrLysProAspSerTyrProLeuPheAspGlyIlePheCysSerAM AM
1141  TGTGAATGTACTAAACCTGATTCTTATCCACTTTTCGATGGTATTTTCTGCAGTTAGTAG
      ACACTTACATGATTTGGACTAAGAATAGGTGAAAAGCTACCATAAAAGACGTCAATCATC

      1159 BSABI, 1188 PSTI, 1200 SALI,

1201  TCGACCCTTGGAAGGATCC
      AGCTGGGAACCTTCCTAGG

      1214 BAMHI,

1261
```

FIG._7C

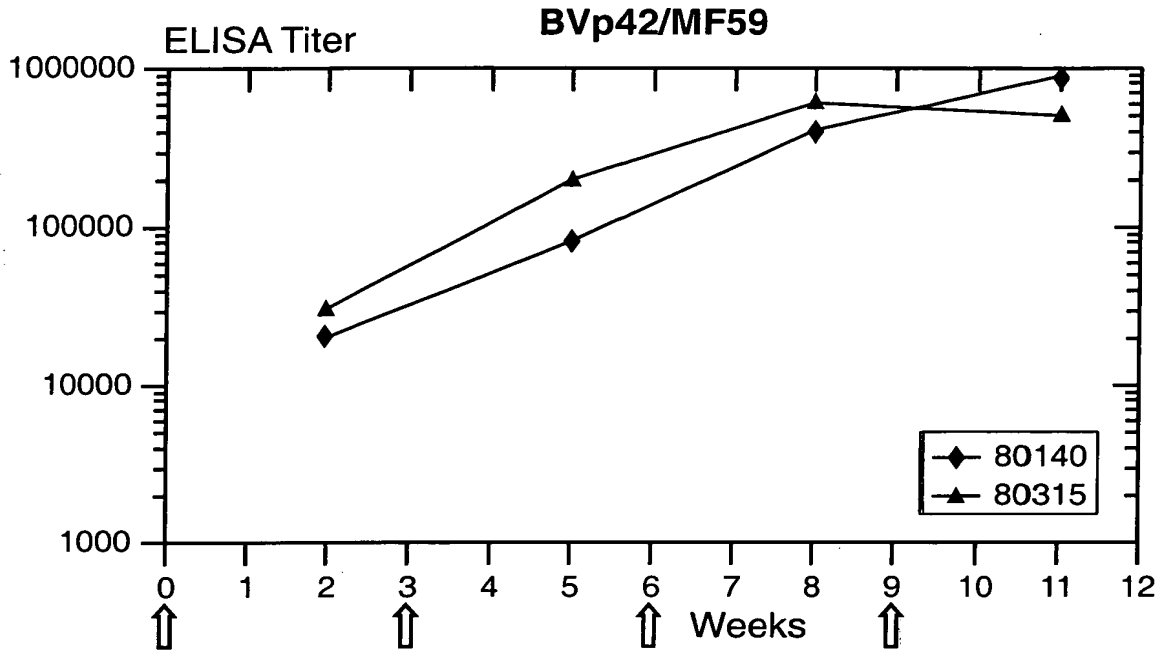


FIG._8A

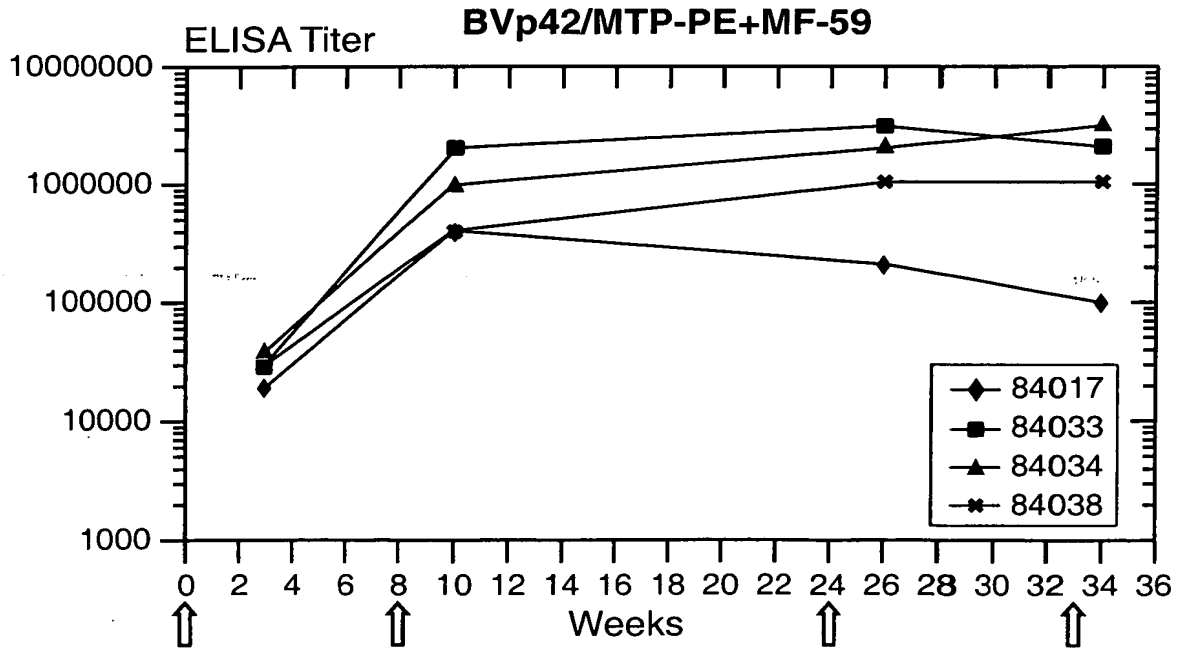


FIG._8B

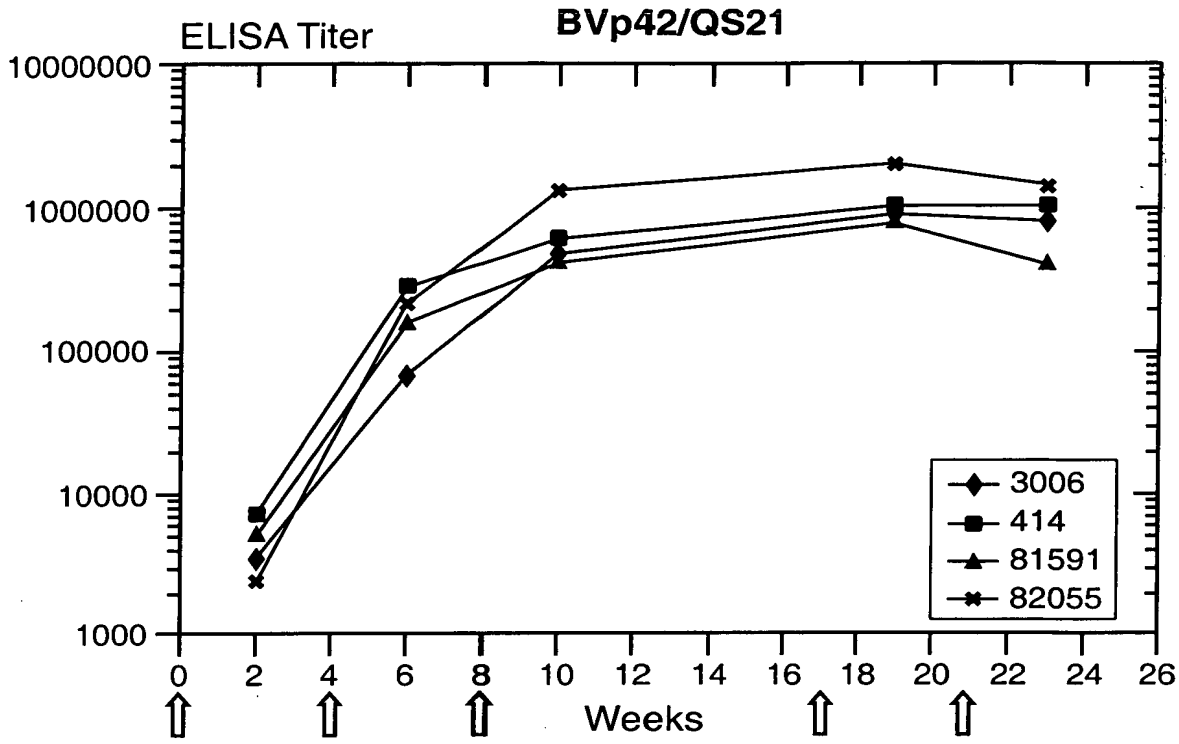


FIG._8C

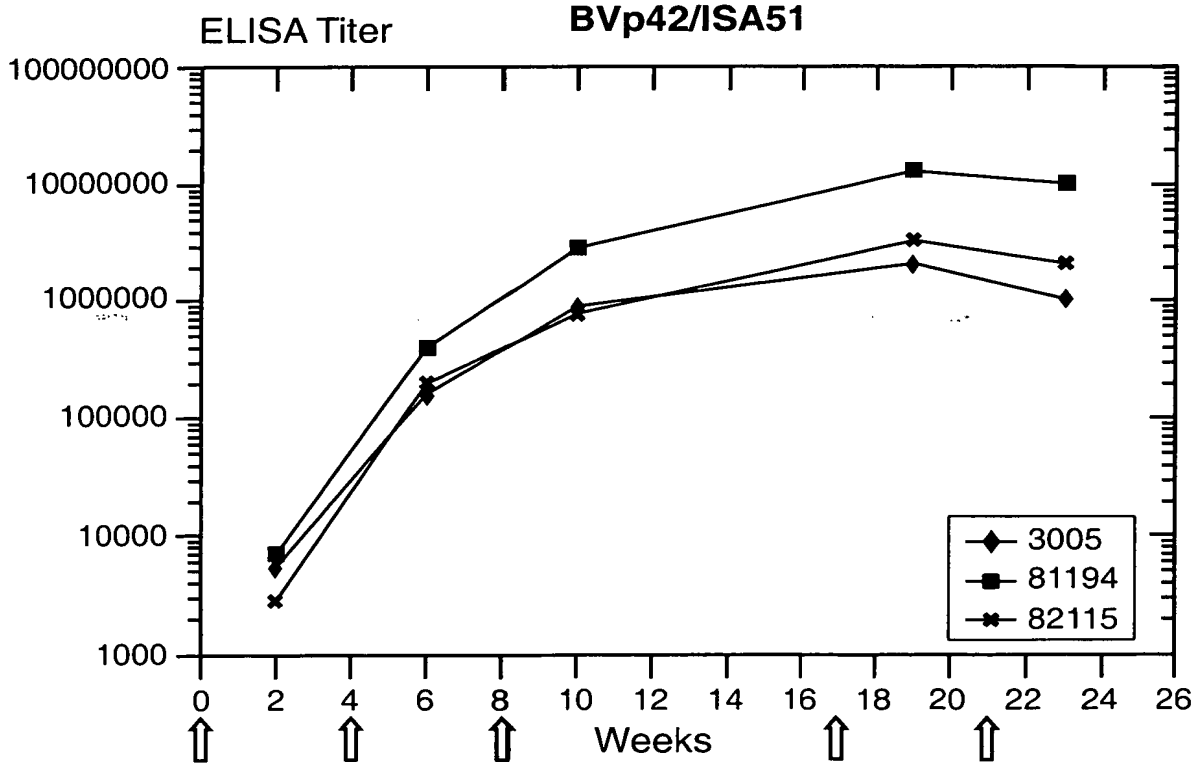


FIG._8D

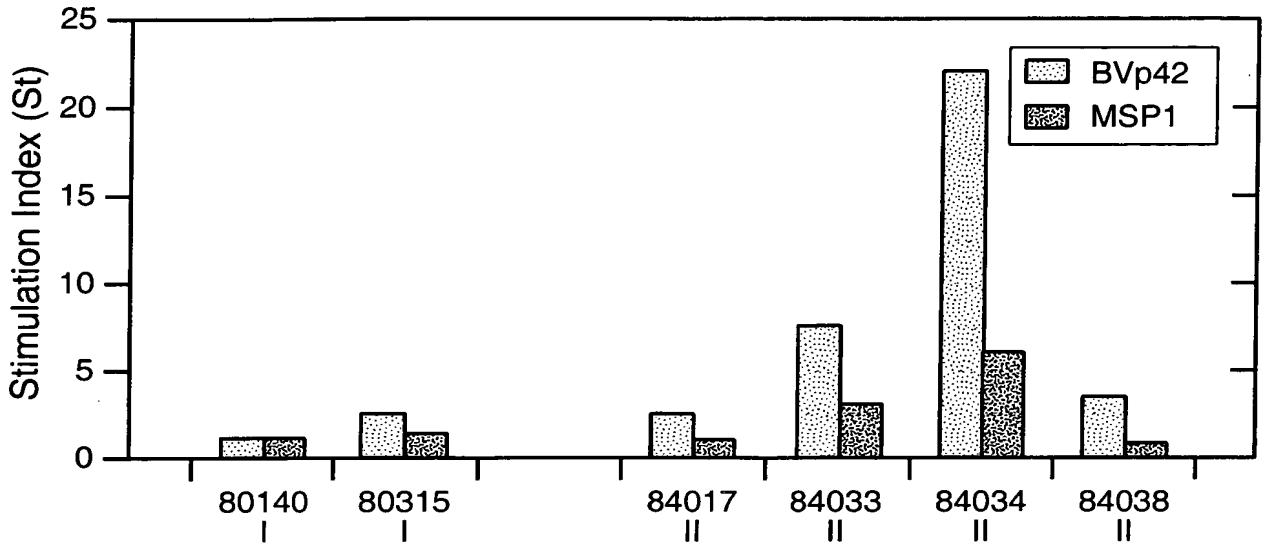


FIG._9

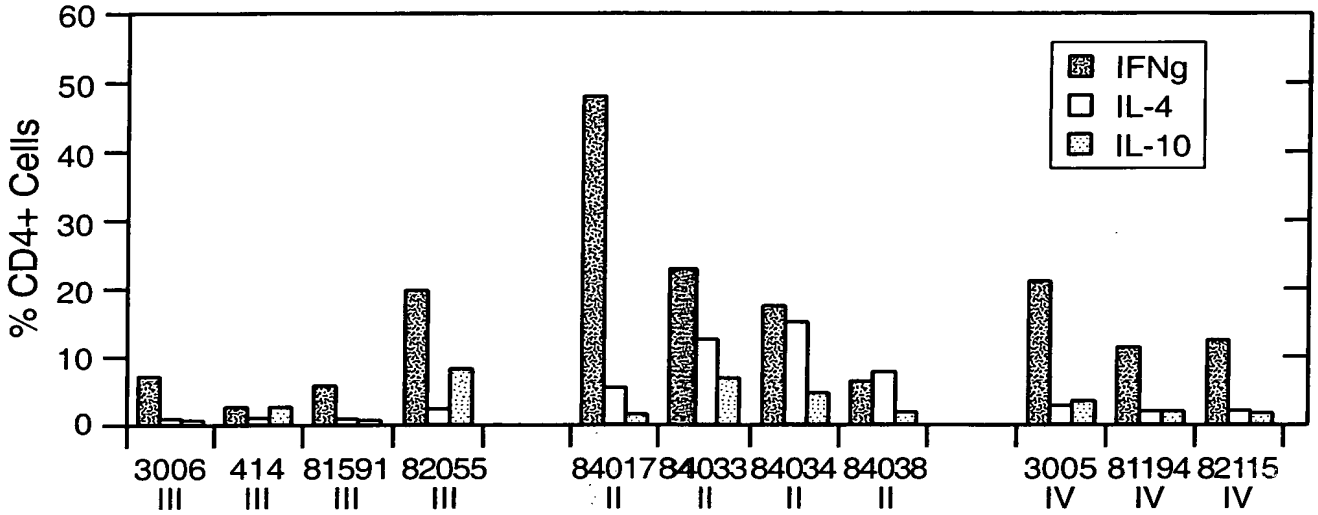


FIG._10A

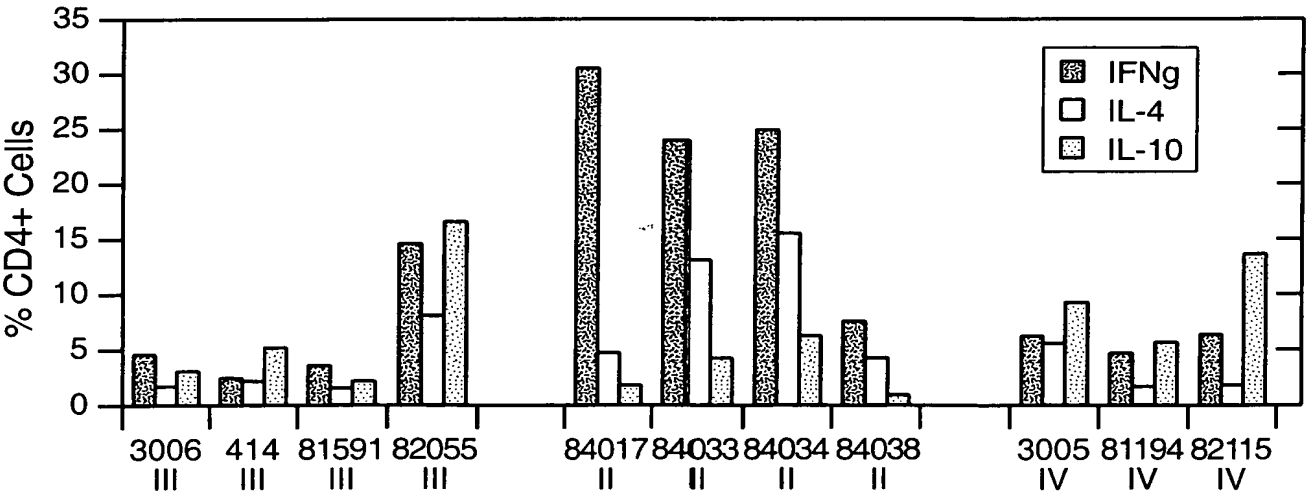


FIG._10B

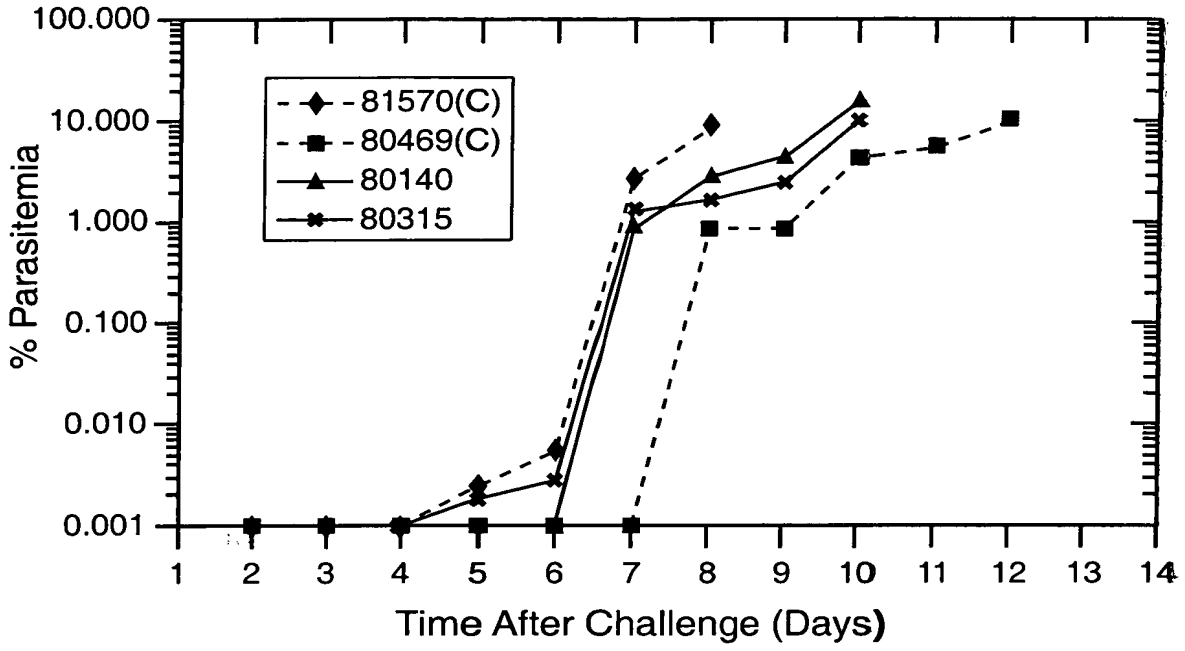
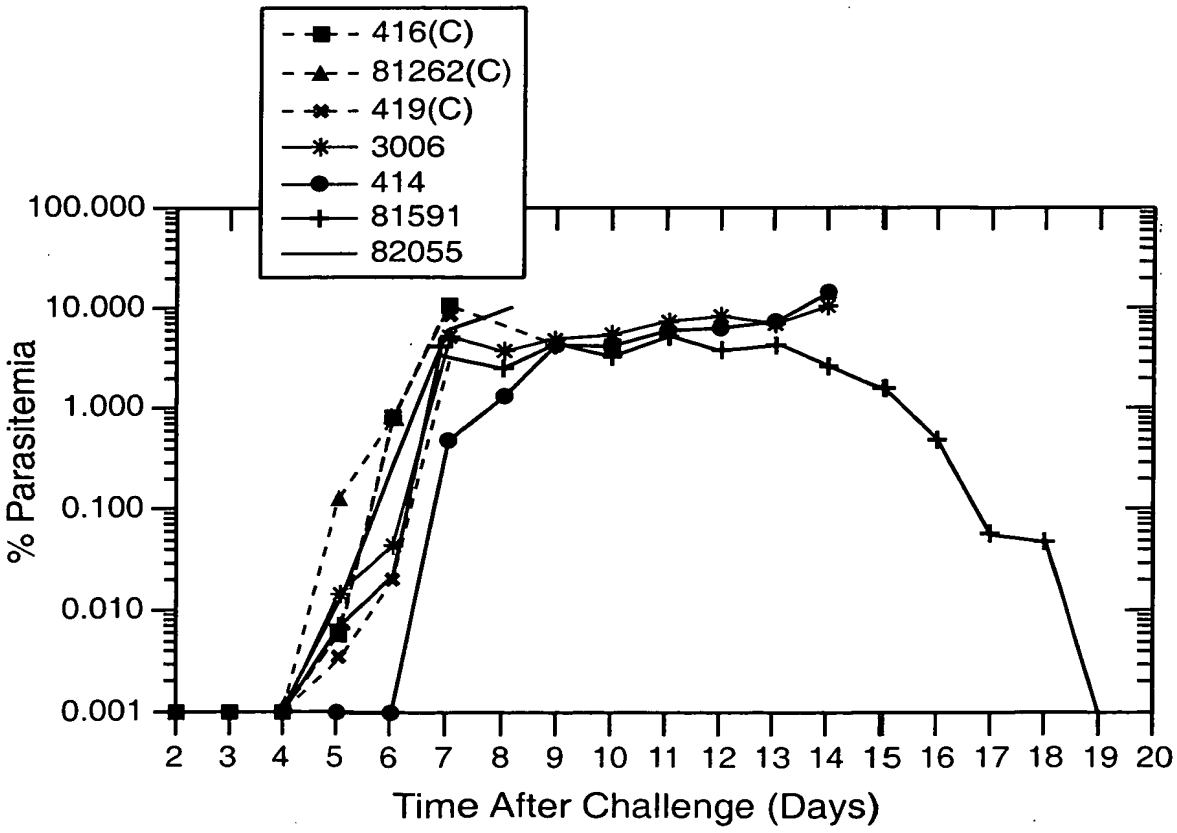


FIG._11A



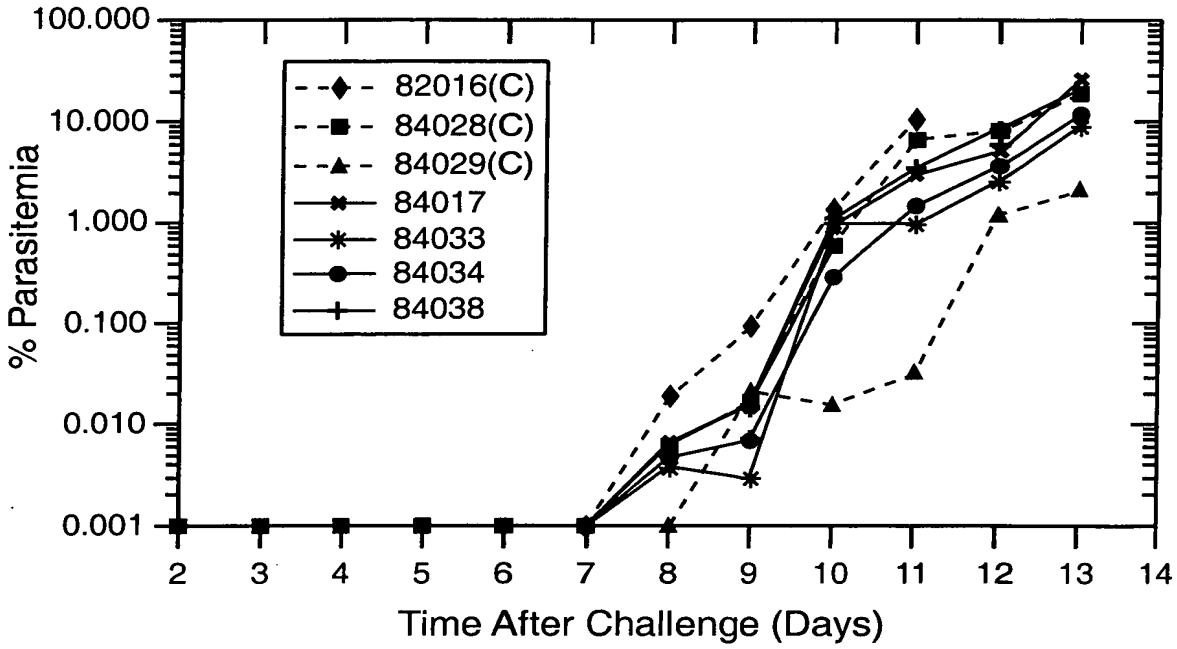


FIG._11C

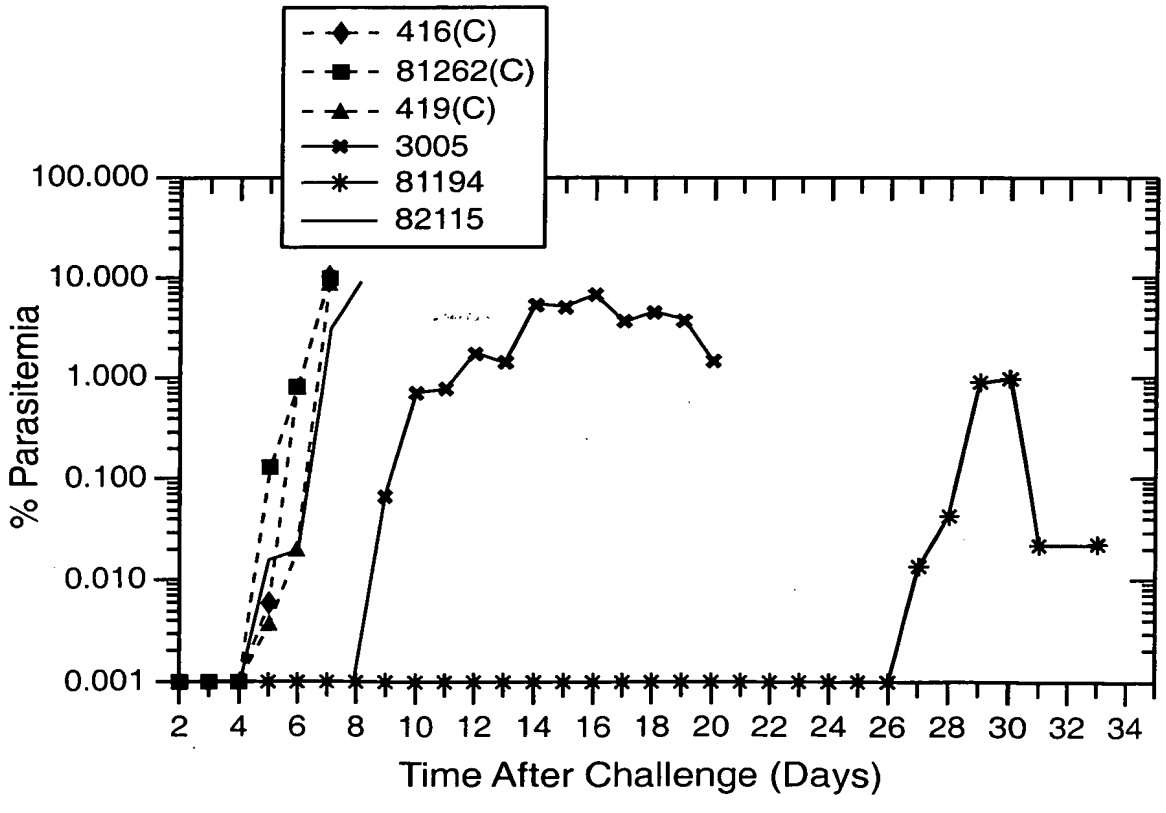


FIG._11D

DNA AND AMINO ACID SEQUENCE OF BVp42-M

```
attggatccactaaa

  13 atgtggtcttggaagtgtcttttattctgggctgtcttggtgacc
     M  W  S  W  K  C  L  L  F  W  A  V  L  V  T
  58 gccactctttgcacagcagcgatctctgttactatggacaacatc
     A  T  L  C  T  A  A  I  S  V  T  M  D  N  I
 103 ctcagtggcttcgagaacgagtacgacgtaatctacctaaagccc
     L  S  G  F  E  N  E  Y  D  V  I  Y  L  K  P
 148 cttgccggtgtctaccgttcattgaagaaacagatagaaaagaat
     L  A  G  V  Y  R  S  L  K  K  Q  I  E  K  N
 193 attttcacgttcaacctcaacctaaatgacatcctcaactcgcgc
     I  F  T  F  N  L  N  L  N  D  I  L  N  S  R
 238 ctcaagaagcgaaaatacttcctcgacgtgttggaatccgacctt
     L  K  K  R  K  Y  F  L  D  V  L  E  S  D  L
 283 atgcaatttaagcacattagctctaacgagtacatcatagaggac
     M  Q  F  K  H  I  S  S  N  E  Y  I  I  E  D
 328 agcttcaagctcttgaattcagaacagaagaacaccctcctaaag
     S  F  K  L  L  N  S  E  Q  K  N  T  L  L  K
 373 tcctacaaatacattaaggagtctgttgagaacgacatcaagttc
     S  Y  K  Y  I  K  E  S  V  E  N  D  I  K  F
 418 gcccaggaaggaattagctactatgagaaagtcctggctaaatac
     A  Q  E  G  I  S  Y  Y  E  K  V  L  A  K  Y
 463 aaggacgacttggaaagcattaagaaggtaatcaaagaagagaag
     K  D  D  L  E  S  I  K  K  V  I  K  E  E  K
 508 gaaaagtttccgagctctccacccacaactcccccatcgcctgca
     E  K  F  P  S  S  P  P  T  T  P  P  S  P  A
 553 aagaccgacgagcagaaaaaagaaagtaagttccttccattcctc
     K  T  D  E  Q  K  K  E  S  K  F  L  P  F  L
 598 accaacatcgaaactctatataacaacctggtgaacaagattgat
     T  N  I  E  T  L  Y  N  N  L  V  N  K  I  D
 643 gactacttaatcaacttgaaggcgaaaattaatgactgtaacgtc
     D  Y  L  I  N  L  K  A  K  I  N  D  C  N  V
 688 gaaaaggatgaagcccacgttaagatcaccaagctttccgatctc
     E  K  D  E  A  H  V  K  I  T  K  L  S  D  L
 733 aaagccatcgacgataagattgacctgtttaagaaccacaacgat
     K  A  I  D  D  K  I  D  L  F  K  N  H  N  D
 778 ttcgacgcaatcaaaaagttgatcaacgacgatactaagaaagac
     F  D  A  I  K  K  L  I  N  D  D  T  K  K  D
 823 atgcttggaaaactgctgtcgacaggcttggtccaaaacttcccg
     M  L  G  K  L  L  S  T  G  L  V  Q  N  F  P
 868 aacaccattataagcaagctgatcgaaggaaagtttcaggatatg
```

FIG. 12A

```
        N  T  I  I  S  K  L  I  E  G  K  F  Q  D  M
  913 ctgaacatctctcagcatcaatgcgtgaagaagcaatgtcccgag
        L  N  I  S  Q  H  Q  C  V  K  K  Q  C  P  E
  958 aattcaggttgcttccgccacttagacgaaagggaggaatgtaaa
        N  S  G  C  F  R  H  L  D  E  R  E  E  C  K
 1003 tgcctgctgaattataaacaggaaggagacaagtgcgtagagaat
        C  L  L  N  Y  K  Q  E  G  D  K  C  V  E  N
 1048 cctaacccaacctgtaacgaaaataacggtggctgcgatgctgac
        P  N  P  T  C  N  E  N  N  G  G  C  D  A  D
 1093 gctaagtgtaccgaggaggacagcggttccaatggcaagaaaata
        A  K  C  T  E  E  D  S  G  S  N  G  K  K  I
 1138 acttgcgaatgcacgaagcccgatagttaccctctcttcgacggt
        T  C  E  C  T  K  P  D  S  Y  P  L  F  D  G
 1183 atcttctgctcc
        I  F  C  S

ccacctcatcatcatcatcattaataaggtaccta
P  P  H  H  H  H  H  H  *  *
```

FIG._12B

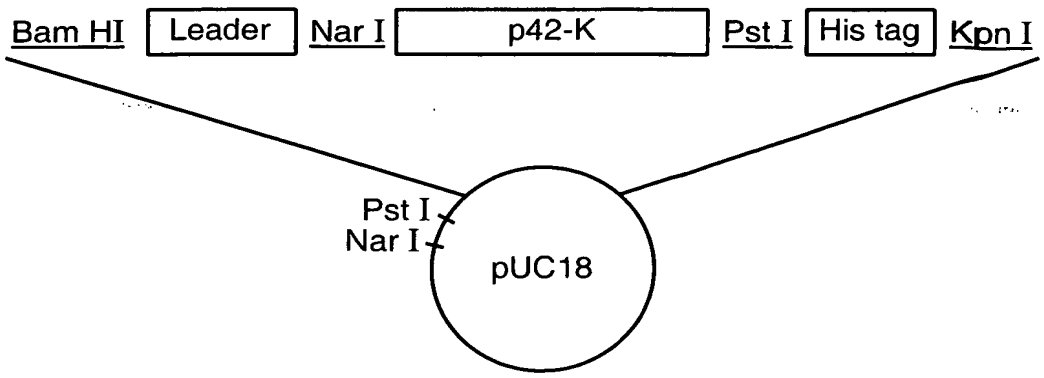


FIG._13

DNA AND AMINO ACID SEQUENCE OF P42-K

```
   1 GGATCCCTAAAATGTGGAGCTGGAAGTGCCTCCTCTTCTGGGCTGTCCTG
                M  W  S  W  K  C  L  L  F  W  A  V  L
  51 GTCACAGCCACACTCTGCACCGCGGGCGCCGCAGTAACTCCTTCCGTAAT
     V  T  A  T  L  C  T  A  G  A  A  V  T  P  S  V  I
 101 TGATAACATACTTTCTAAAATTGAAAATGAATATGAGGTTTTATATTTAA
     D  N  I  L  S  K  I  E  N  E  Y  E  V  L  Y  L
 151 AACCTTTAGCAGGTGTTTATAGAAGTTTAAAAAAACAATTAGAAAATAAC
     K  P  L  A  G  V  Y  R  S  L  K  K  Q  L  E  N  N
 201 GTTATGACATTTAATGTTAATGTTAAGGATATTTTAAATTCACGATTTAA
     V  M  T  F  N  V  N  V  K  D  I  L  N  S  R  F  N
 251 TAAACGTGAAAATTTCAAAAATGTTTTAGAATCAGATTTAATTCCATATA
      K  R  E  N  F  K  N  V  L  E  S  D  L  I  P  Y
 301 AAGATTTAACATCAAGTAATTATGTTGTCAAAGATCCATATAAATTTCTT
     K  D  L  T  S  S  N  Y  V  V  K  D  P  Y  K  F  L
 351 AATAAAGAAAAAAGAGATAAATTCTTAAGCAGTTATAATTATATTAAGGA
      N  K  E  K  R  D  K  F  L  S  S  Y  N  Y  I  K  D
 401 TTCAATAGATACGGATATAAATTTTGCAAATGATGTTCTTGGATATTATA
       S  I  D  T  D  I  N  F  A  N  D  V  L  G  Y  Y
 451 AAATATTATCCGAAAAATATAAATCAGATTTAGATTCAATTAAAAAATAT
     K  I  L  S  E  K  Y  K  S  D  L  D  S  I  K  K  Y
 501 ATCAACGACAAACAAGGTGAAAATGAGAAATACCTTCCCTTTTTAAACAA
      I  N  D  K  Q  G  E  N  E  K  Y  L  P  F  L  N  N
 551 TATTGAGACCTTATATAAAACAGTTAATGATAAAATTGATTTATTTGTAA
       I  E  T  L  Y  K  T  V  N  D  K  I  D  L  F  V
 601 TTCATTTAGAAGCAAAAGTTCTAAATTATACATATGAGAAATCAAACGTA
     I  H  L  E  A  K  V  L  N  Y  T  Y  E  K  S  N  V
 651 GAAGTTAAAATAAAAGAACTTAATTACTTAAAAACAATTCAAGACAAATT
      E  V  K  I  K  E  L  N  Y  L  K  T  I  Q  D  K  L
 701 GGCAGATTTTAAAAAAAATAACAATTTCGTTGGAATTGCTGATTTATCAA
       A  D  F  K  K  N  N  N  F  V  G  I  A  D  L  S
 751 CAGATTATAACCATAATAACTTATTGACAAAGTTCCTTAGTACAGGTATG
     T  D  Y  N  H  N  N  L  L  T  K  F  L  S  T  G  M
```

FIG. 14A

```
801 GTTTTTGAAAATCTTGCTAAAACCGTTTTATCTAATTTACTTGATGGAAA
     V  F  E  N  L  A  K  T  V  L  S  N  L  L  D  G  N
851 CTTGCAAGGTATGTTAAACATTTCACAACACCAATGCGTAAAAAAACAAT
     L  Q  G  M  L  N  I  S  Q  H  Q  C  V  K  K  Q
901 GTCCACAAAATTCTGGATGTTTCAGACATTTAGATGAAAGAGAAGAATGT
     C  P  Q  N  S  G  C  F  R  H  L  D  E  R  E  E  C
951 AAATGTTTATTAAATTACAAACAAGAAGGTGATAAATGTGTTGAAAATCC
     K  C  L  L  N  Y  K  Q  E  G  D  K  C  V  E  N  P
1001 AAATCCTACTTGTAACGAAAATAATGGTGGATGTGATGCAGATGCCAAAT
      N  P  T  C  N  E  N  N  G  G  C  D  A  D  A  K
1051 GTACCGAAGAAGATTCAGGTAGCAACGGAAAGAAAATCACATGTGAATGT
     C  T  E  E  D  S  G  S  N  G  K  K  I  T  C  E  C
1101 ACTAAACCTGATTCTTATCCACTTTTCGATGGTATTTTCTGCAGTCATCA
      T  K  P  D  S  Y  P  L  F  D  G  I  F  C  S  H  H
1151 TCATCATCATCATTAATAAGGTACC
      H  H  H  H  *  *
```

Underlined sequences represent restriction sites.
Bold letters represent alterations done to the leader sequence as described in the methods.
The boxed letter represents the original sequence where a mis-sense mutation to a cytosine occurred.
"*" represent stop codons.

FIG._14B

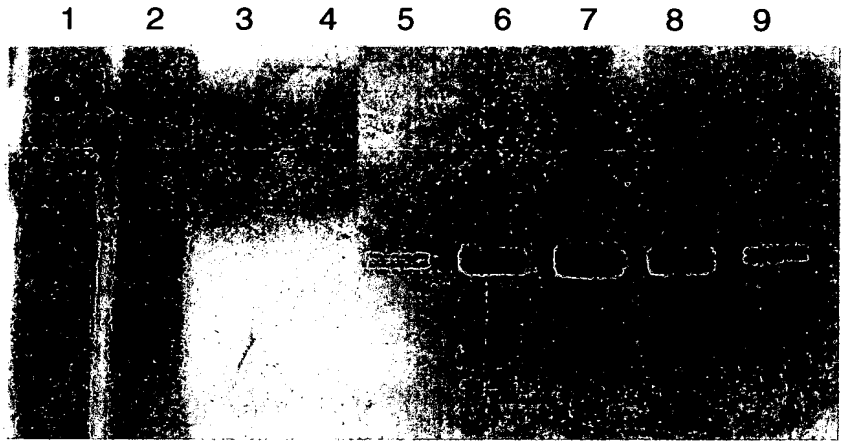


FIG._15

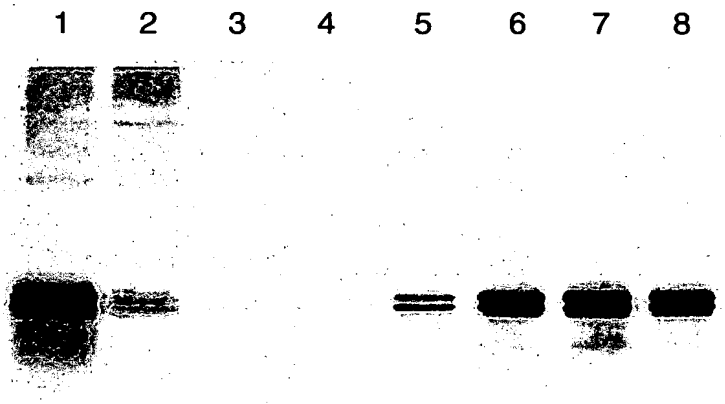


FIG._16

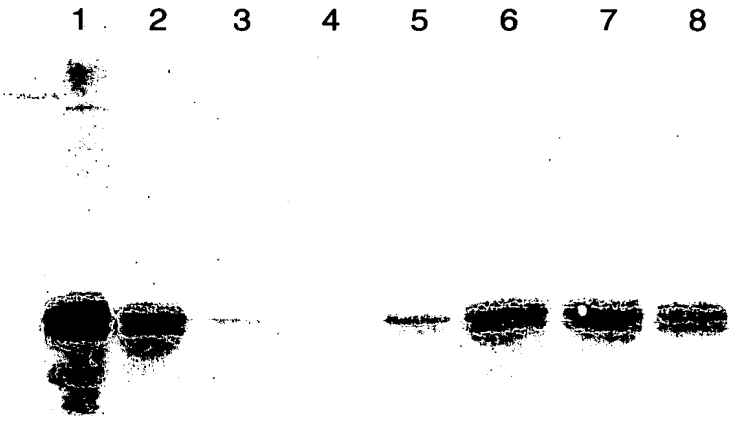


FIG._17

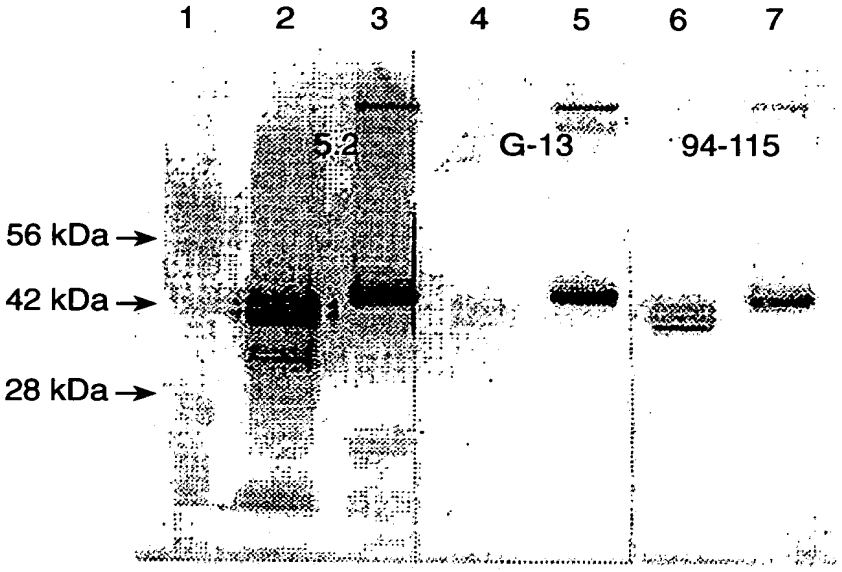


FIG._18A

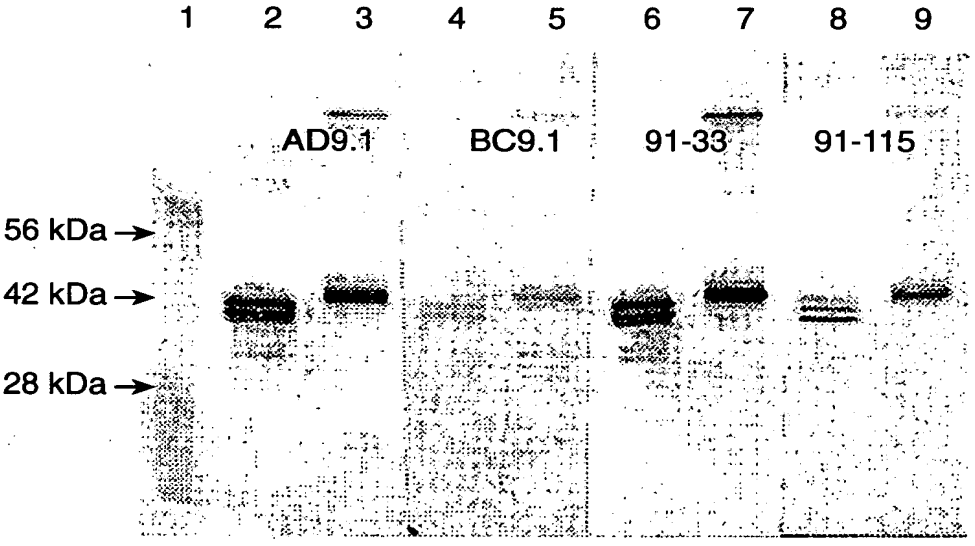


FIG._18B